**AMENDMENTS TO THE CLAIMS:**

Amend the claims as follows:

Claims 1-23 cancelled.

24. (Currently Amended) A method of analysing a library of polynucleotides, said polynucleotides being contained in cloning vectors having a particular host range, the method comprising (i) selecting cloning vectors in the library which contain a polynucleotide having a particular characteristic, (ii) modifying said selected cloning vectors to allow a transfer and integration of said vectors and/or of the polynucleotide which they contain into ~~the genome~~ a chromosome of a selected host cell, and (iii) analysing the polynucleotides contained in said modified vectors upon transfer of said modified vectors into said selected host cell.

25. (Previously Presented) The method of claim 24, wherein the library comprises a plurality of unknown polynucleotides.

26. (Previously Presented) The method of claim 24, wherein the library comprises a plurality of environmental DNA fragments.

27. (Previously Presented) The method of claim 24, wherein the cloning vectors of the library are *E. coli* cloning vectors.

28. (Previously Presented) The method of claim 24, wherein the selected cloning vectors are modified by targeted insertion, into the vectors, of a target polynucleotide construct.

29. (Previously Presented) The method of claim 28, wherein the targeted insertion is performed in a region of the selected cloning vectors distinct from the polynucleotide having a particular characteristic.

30. (Currently Amended) The method of claim 28, wherein the target polynucleotide construct comprises [[an]]a functional origin of transfer ~~functional~~ in the selected host cell.

31. (Previously Presented) The method of claim 30, wherein the origin of transfer is functional in *E. coli* host cells.

32. (Currently Amended) The method of claim 31, wherein the origin of transfer is an origin of transfer contained in a plasmid selected from the group consisting of RP4, pTiC58, F, RSF1010[[, ColE1]] and R6K($\alpha$).

33. (Previously Presented) The method of claim 28, wherein the target polynucleotide construct comprises an integrase functional in the selected host cell.

34. (Previously Presented) The method of claim 33, wherein the integrase is ϕC31 integrase.

35. (Previously Presented) The method of claim 29, wherein the target polynucleotide construct comprises a transcriptional promoter functional in the selected host cell.

36. (Previously Presented) The method of claim 28, wherein the target polynucleotide construct comprises a transposable nucleic acid construct.

37. (Previously Presented) The method of claim 36, wherein the transposable nucleic acid comprises, two inverted repeats, the target polynucleotide construct and a marker gene, said inverted repeats flanking the target polynucleotide construct and the marker gene.

38. (Previously Presented) The method of claim 24, wherein the cloning vector comprises a first marker gene and wherein, in step ii), the cloning vector is modified by:

contacting in vitro, in the presence of a transposase, the selected cloning vectors with a transposon comprising, two inverted repeats, the target polynucleotide construct and a second marker gene distinct from the first marker gene with inverted repeats flanking the target polynucleotide construct and the second marker gene, and

selecting the cloning vectors which have acquired the second marker gene and which have lost the first marker gene.

39. (Previously Presented) The method of claim 24, wherein, in step (i), the cloning vectors which contain a polynucleotide having a particular characteristic are selected by molecular screening.

40. (Previously Presented) The method of claim 24, wherein, in step (iii), the modified cloning vectors are transferred into the selected host cell by conjugative transfer.

41. (Previously Presented) The method of claim 24, wherein, in step (iii), polynucleotides are analysed by determining the phenotype or properties of the host cell upon transfer or expression of the modified vector.

42. (Previously Presented) A method for the identification or cloning of polynucleotides encoding a selected phenotype, the method comprising (i) cloning environmental DNA fragments into *E.coli* cloning vectors to produce a metagenomic library, (ii) identifying or selecting cloning vectors in said library which contain DNA fragments having a particular characteristic of interest, (iii) modifying the identified or selected cloning vectors into shuttle or expression vectors for transfer and integration in a selected host cell, (iv) transferring the modified cloning vectors into said selected host

cell and (v) identifying or cloning the DNA fragments contained in said modified cloning vectors which encode said selected phenotype in said selected host cell.

43. (Withdrawn) A transposable nucleic acid construct, wherein said construct comprises an origin of transfer and elements for integration and selection in a selected host cell genome flanked by two inverted repeats.

44. (Withdrawn) A library of polynucleotides, wherein said library comprises a plurality of environmental DNA fragments cloned into cloning vectors, wherein said environmental DNA fragments contain a common molecular characteristic and wherein said cloning vectors are *E. coli* cloning vectors comprising a target polynucleotide construct allowing transfer and integration of the environmental DNA into a selected host cell distinct from *E. coli.*

45. (Withdrawn) A polynucleotide sequence comprising all or part of SEQ ID NOs: 1 or 2, or of their complementary strand.

46. (Withdrawn) An oligonucleotide comprising SEQ ID NO: 3 or 4.

47. (Previously Presented) The method of claim 27, wherein the vectors are selected from the group consisting of a cosmid, a fosmid, P1 and BAC vectors.